

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 1, 2001, 16:17:16 ; Search time 52.57 Seconds  
(without alignments)  
147.151 Million cell updates/sec

Title: US-09-331-631A-24\_COPY\_29\_94  
Perfect score: 382  
Sequence: 1 HDEDDRRGSHLQOCVORC.....EQEEDGRCRGWHEGGEREE 66

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 374700 segs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SPREMBL\_15:\*  
2: sp\_archaea:\*  
3: sp\_bacteria:\*  
4: sp\_fungi:\*  
5: sp\_human:\*  
6: sp\_invertebrate:\*  
7: sp\_mhnc:\*  
8: sp\_mammal:\*  
9: sp\_organelle:\*  
10: sp\_phage:\*  
11: sp\_plant:\*  
12: sp\_rodent:\*  
13: sp\_virus:\*  
14: sp\_vertebrate:\*  
15: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	382	100.0	637	10 Q03678	Q03678 hordeum vul
2	138	36.1	582	10 Q03865	Q03865 zea mays (m
3	136	35.6	238	10 Q01257	Q01257 zea luxuria
4	135	35.3	238	10 Q01249	Q01249 zea mays su
5	135	35.3	238	10 Q01255	Q01255 zea mays su
6	135	35.3	238	10 Q05BE8	Q05BE8 zea mays su
7	135	35.3	240	10 Q05BF0	Q05BF0 zea mays su
8	135	35.3	240	10 Q05BE9	Q05BE9 zea mays su
9	135	35.3	242	10 Q01251	Q01251 zea mays su
10	135	35.3	242	10 Q05BE5	Q05BE5 zea mays su
11	135	35.3	407	10 Q01750	Q01750 zea mays (m
12	134	35.1	238	10 Q05BE5	Q05BE5 zea luxuria
13	134	35.1	238	10 Q05626	Q05626 zea luxuria
14	133	34.8	238	10 Q01258	Q01258 zea luxuria
15	133	34.8	240	10 Q01252	Q01252 zea mays su
16	133	34.8	240	10 Q01256	Q01256 zea mays su
17	133	34.8	240	10 Q05BE7	Q05BE7 zea mays su
18	133	34.8	540	10 Q03BE6	Q03BE6 zea mays (m
19	132	34.6	239	10 Q05BF1	Q05BF1 zea mays su

20	130	34.0	239	10 Q01253	Q01253 zea mays su
21	129.5	33.9	122	10 Q03863	Q03863 zea mays (m
22	127	33.2	236	10 Q01254	Q01254 zea mays su
23	125.5	32.9	246	10 Q01261	Q01261 tripacum d
24	125	32.7	236	10 Q05BE2	Q05BE2 zea mays su
25	124.5	32.6	242	10 Q01260	Q01260 tripacum d
26	116	30.4	236	10 Q01250	Q01250 zea mays su
27	115	30.1	666	10 Q05PL5	Q05PL5 macadamia i
28	111.5	29.2	242	10 Q01259	Q01259 tripacum d
29	105	27.5	666	10 Q05PL4	Q05PL4 macadamia i
30	97	25.4	393	10 Q027P0	Q027P0 oryza sativ
31	92	24.1	625	11 Q09053	Q09053 ratius norv
32	91	23.8	402	10 Q02RH8	Q02RH8 oryza sativ
33	91	23.3	625	10 Q05PL3	Q05PL3 macadamia i
34	85	22.3	593	10 Q05EM4	Q05EM4 juglans reg
35	76.5	20.0	566	10 Q02494	Q02494 pisum sativ
36	75	19.6	512	5 Q09VRD5	Q09VRD5 drosophila
37	75	19.6	699	4 Q04769	Q04769 homo sapien
38	74.5	19.5	1655	5 Q04754	Q04754 drosophila
39	73.5	19.2	239	12 Q09ME3	Q09ME3 avian endog
40	73.5	19.2	261	13 Q03368	Q03368 xenopus lae
41	73.5	19.2	810	10 Q02W13	Q02W13 cucurbita m
42	73	19.1	532	2 Q052993	Q052993 escherichia
43	72	18.8	525	10 Q04358	Q04358 theobroma c
44	72	18.8	818	5 Q09VJ77	Q09VJ77 drosophila
45	71	18.6	57	4 Q094J1	Q094J1 homo sapien

## ALIGNMENTS

RESULT 1  
ID Q03678 PRELIMINARY: PRT: 637 AA.

AC Q03678; 01-NOV-1996 (TREMUREL.01, Created)  
DT 01-NOV-1996 (TREMUREL.01, Last sequence update)  
DT 01-OCT-2000 (TREMUREL.15, Last annotation update)  
DE FERTIL STORAGE PROTEIN.  
GN BEG1 OR GBL1.  
OS Hordeum vulgare (Barley), and Triticum aestivum (Wheat).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Hordeum.  
OX NCBI\_Taxid=4513; 4565;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93287986; PubMed=8510647;  
RA Heck G.R., Chamberlain A.C., Ho T.H.D.;  
RT "Barley embryo globulin 1 gene, Beg1: characterization of cDNA,  
RT chromosome mapping and regulation of expression.";  
RL Mol. Gen. Genet. 239:209-218(1993).  
DR EMBL: M64372; AAA32936.1; -;  
DR EMBL: M61712; AAA34269.1; -;  
DR HSSP: P02853; 2PHL.  
DR MENDEL: 8553; Horvu:1188; 8553.  
DR INTERPRO: IPR000901; -;  
DR INTERPRO: IPR001113; -;  
DR PRAM: PF00546; Seedstore\_7s; 1.  
DR PROSITE: PS00867; CPASASE\_2; UNKNOWN\_1.  
DR PRODOM: PD081059; -; 1.  
KW Seed storage protein.  
SQ SEQUENCE 637 AA; 72252 MW; F323F4FF99947C3C CRC64;

Query Match 100.0%; Score 382; DB 10; Length 637;  
Best Local Similarity 100.0%; Pred. No. 7.4e-37;  
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDEDDRRGSHLQOCVORCROEPRYSHARVOECDDDOOHGRHGEFEQGRGRMG 60  
Db 29 HDEDDRRGSHLQOCVORCROEPRYSHARVOECDDDOOHGRHGEFEQGRGRMG 88  
QY 61 EGEREE 66

Db 89 EGEREE 94

RESULT 2  
003865 PRELIMINARY; PRT; 582 AA.

ID 003865;  
AC 003865;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, last sequence update)  
DT 01-OCT-2000 (TReMBLrel. 15, last annotation update)  
DE VITCLIN-LIKE EMBRYO STORAGE PROTEIN.

GN GIB1-L.  
OS Zea mays (maize).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.  
OX NCBI\_TaxId=4577;  
RN 11  
RP SEQUENCE FROM N.A.  
RC STRAIN-W64A;  
RX MEDLINE-92090707; PubMed-1752424;  
RA Belanger F.C., Kriz A.L.;

RT "Molecular basis for allelic polymorphism of the maize Globulin-1 gene.";

RL Genetics 129:863-872(1991).  
DR EMBL; X59083; CAA1809.1; -.  
DR HSSP; P50477; ICAU.  
DR MENDEL; 11234; Zeama; 1188; 11234.

DR INTERPRO; IPR000901; -.  
DR INTERPRO; IPR001113; -.  
DR PRAM; PR00546; Seedstore\_7s; 1.  
DR PROSITE; PS00867; CPSASE\_2; UNKNOWN\_1.  
DR PRODOM; PD081059; -; 1.  
KW Seed storage protein.

SO SEQUENCE 582 AA; 66162 MW; 680D85FEC07CB885 CRC64;

Query Match 36.1%; Score 138; DB 10; Length 582;  
Best Local Similarity 37.7%; Pred. No. 2e-08;  
Matches 26; Conservative 14; Mismatches 21; Indels 8; Gaps 3;

OY 2 DDEDDRGGHSLOQVORCROERPRYSHARCVOECRDDQ----QOGRHNEDEEGCGRG 57  
DB 26 DDNNHHHGKSGRCVYARC-EDRPWHORPCLQCREREKROERSRHADDSRGSS-- 82

OY 58 WHGEGEREE 66  
DB 83 -SSEDEREQ 90

RESULT 3  
081257 PRELIMINARY; PRT; 238 AA.

AC 081257;  
DT 01-NOV-1998 (TReMBLrel. 08, Created)  
DT 01-NOV-1998 (TReMBLrel. 08, last sequence update)  
DT 01-OCT-2000 (TReMBLrel. 15, last annotation update)  
DE GLOBULIN-1 (FRAGMENT).

OS Zea luxurians (Teosinte).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.  
OX NCBI\_TaxId=15945;  
RN 11  
RP SEQUENCE FROM N.A.  
RA Hilton H., Gaut B.S.;

RT "Speciation and domestication in maize and its wild relatives: evidence from the Globulin-1 gene.";

RL Genetics 0:0-0(1998).  
DR EMBL; AF064228; AAC31471.1; -.  
DR HSSP; P50477; ICAU.  
DR MENDEL; 31899; Zealu; 1188; 31899.  
DR INTERPRO; IPR000901; -.  
DR INTERPRO; IPR001113; -.

DR PRAM; PR00546; Seedstore\_7s; 1.  
DR PROSITE; PS00867; CPSASE\_2; UNKNOWN\_1.  
FT NON\_TER 238  
SQ SEQUENCE 238 AA; 27233 MW; FD31A8066738E68 CRC64;

Query Match 35.6%; Score 136; DB 10; Length 238;  
Best Local Similarity 36.2%; Pred. No. 1.6e-08;  
Matches 25; Conservative 16; Mismatches 20; Indels 8; Gaps 3;

OY 2 DDEDDRGGHSLOQVORCROERPRYSHARCVOECRDDQ----QOGRHNEDEEGCGRG 57  
DB 26 DDNNHHHGKSGRCVYARC-EDRPWHORPCLQCREREKROERSRHADDSRGSS-- 82

OY 58 WHGEGEREE 66  
DB 83 -SSEDEREQ 90

RESULT 4  
081249 PRELIMINARY; PRT; 238 AA.

ID 081249;  
AC 081249;  
DT 01-NOV-1998 (TReMBLrel. 08, Created)  
DT 01-NOV-1998 (TReMBLrel. 08, last sequence update)  
DT 01-OCT-2000 (TReMBLrel. 15, last annotation update)  
DE GLOBULIN-1 (FRAGMENT).

OS Zea mays subsp. mays (maize).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.  
OX NCBI\_TaxId=4578;  
RN 11  
RP SEQUENCE FROM N.A.  
RA Hilton H., Gaut B.S.;

RT "Speciation and domestication in maize and its wild relatives: evidence from the Globulin-1 gene.";

RL Genetics 0:0-0(1998).  
DR EMBL; AF064212; AAC31455.1; -.  
DR HSSP; P50477; ICAU.  
DR MENDEL; 31891; Zeama; 1188; 31891.

DR INTERPRO; IPR000901; -.  
DR INTERPRO; IPR001113; -.  
DR PRAM; PR00546; Seedstore\_7s; 1.  
DR PROSITE; PS00867; CPSASE\_2; UNKNOWN\_1.  
FT NON\_TER 238  
SQ SEQUENCE 238 AA; 27298 MW; EDF6A1DE3F86D0F0 CRC64;

Query Match 35.3%; Score 135; DB 10; Length 238;  
Best Local Similarity 36.2%; Pred. No. 2e-08;  
Matches 25; Conservative 16; Mismatches 22; Indels 6; Gaps 3;

OY 2 DDEDDRGGHSLOQVORCROERPRYSHARCVOECRDDQ----QOGRHNEDEEGCGRG 57  
DB 26 DDNNHHHGKSGRCVYARC-EDRPWHORPCLQCREREKROERSRHADDSRGSS 84

OY 58 WHGEGEREE 66  
DB 85 -EDEDEREQ 92

RESULT 5  
081255 PRELIMINARY; PRT; 238 AA.

ID 081255;  
AC 081255;  
DT 01-NOV-1998 (TReMBLrel. 08, Created)  
DT 01-NOV-1998 (TReMBLrel. 08, last sequence update)  
DT 01-MAY-2000 (TReMBLrel. 13, last annotation update)  
DE GLOBULIN-1 (FRAGMENT).

OS Zea mays subsp. parviglumis.  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.  
OX NCBI\_TaxId=76912;

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RN      [1]
RP      SEQUENCE FROM N.A.
RA      Hilton H., Gaut B.S.;
RT      "Speciation and domestication in maize and its wild relatives:
RT      evidence from the Globulin-1 gene.";
RL      Genetics 0:0-0(1998).
DR      EMBL; AF064224; AAC31467.1; -.
DR      MENDEL; 31897; Zeama;1188;11897.
DR      INTERPRO; IPR000901; -.
DR      INTERPRO; IPR001113; -.
DR      Pfam; PF00546; Seedstore_7s; 1.
DR      PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
FT      NON TER      238
SQ      SEQUENCE      238 AA; 27205 MW; 1186EA5DEEB507E CRC64;

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QY	2	DDEDRRGCHSLDQOVCKRQRPYRSHARCQVQRDD	---	QOQHGHRQEDQEEQCRGKG	57
Db	26	DDNNHHHNGHSGRCVRYK	-EDRPWHQRPCLDCKREKREKQDERSHREADD	RSQEG	-- 82
QY	58	WHGEGRE	65		
Db	83	-SSDEERE	89		

RESULT	6
09SBEB	
ID	09SBEB
AC	PRELIMINARY; PRT; 238 AA.
DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT	01-OCT-2000 (TREMBLrel. 13, last annotation update)
DE	GLOBULIN-1 (FRAGMENT).
OS	zea mays subsp. parviglumis.
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta
OC	Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
OX	NCBI_taxid=76912;
RP	[1]
RN	SEQUENCE FROM N.A.
RA	Hilton H., Gaut B.S.;
RT	"Speciation and domestication in maize and its wild relatives:
RT	evidence from the Globulin-1 gene.";
RL	Genetics 0:0-0(1998).
DR	EMBL; AF064421; AAC31464.1; -.
DR	HSSP; P50477; ICAU.
DR	INTERPRO; IPR000901; -.
DR	INTERPRO; IPR001113; -.
DR	PFAM; PF00546; Seedstore.7s; 1.
DR	PROSITE; PS00867; CPSSSF_2; UNKNOWN_1.
FT	NON_TER
Q	SEQUENCE 238 AA; 27362 MW; A75C0C7DED9B773A CRC64;

Query Match	35.3%	Score 135	DB 10	Length 238
Best Local Similarity	36.2%	Pred. No. 2e-08		
Matches	25	Conservative	16	Mismatches 22
				Indels 6
				Gaps 3
QY	2	DDEDRCGHSLOOCVORCRQERPRYSIARCVQOEKRDQO---	OOHGRIHQDEEQGRGK	57
Db	26	DDNNHHNHGHSKRCVRC-EDRPWQRKCLQCRKEERERKROERSRHADRSKGSS	84	
QY	58	WHGEGREE	66	
Db	85	-EDEREREQ	92	
RESULT	7			
Q9SBF0		PRELIMINARY:	PRT:	240 AA.
Q9SBF0				

AC 095BFO: 01-MAY-2000 (T-EMBLrel. 13, Created)  
DT 01-MAY-2000 (T-EMBLrel. 13, last sequence update)  
DT 01-OCT-2000 (T-EMBLrel. 15, last annotation update)  
DE GLOBULIN-1 (FRAGMENT).  
OS Zea mays subsp. parviglumis.  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta  
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.  
ON NCBI\_TaxID=76912;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA HILTON H., GAUT B.S.;  
RT "Speciation and domestication in maize and its wild relatives:  
RT evidence from the Globulin-1 gene.";  
RL Genetics 0:0-0(1998).  
DR EMBL: AF064219; AAC31462.1; -.  
DR HSSP: P50477; 1CAU.  
DR INTERPRO: IPR000901; -.  
DR INTERPRO: IPR001113; -.  
DR PFAM: PF00546; Seedstora\_7s.1.  
DR PROSITE: PS00867; CPSASE\_2; UNKNOWN\_1.  
FT NON\_TER 240 240  
SQ SEQUENCE 240 AA: 27499 MW: ECDEI13393DC94AAC CRC64:

QY	2	DDEDDRGSHLQOVCRCROERPRYSIARVCQVERDDO----	QONGKHNDEDEEGRGKRG	57
	26	DDNNHHHGGHSGKVCVRKC-EDRPNWQRPCLDQCRDEERKAKRDSRHEADRDSGKSS		84
Db	58	WHGSGEERE	66	
QY	85	-EDEREREQ	92	
Db				

RESULT	8			
09SBEB9				
ID	09SBEB9	PRELIMINARY;	PRT;	240 AA.
AC	09SBEB9;			
DT	01-MAY-2000 (TREMBLrel, 13, Created)			
DT	01-MAY-2000 (TREMBLrel, 13, Last sequence update)			
DT	01-OCT-2000 (TREMBLrel, 15, Last annotation update)			
DE	GLOBULIN-1 (FRAGMENT).			
OS	Zea mays subsp. parviglumis			
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;			
OC	Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.			
OX	NCBI_TaxId=76912;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Hilton H., Gaut B.S.;			
RT	"Speciation and domestication in maize and its wild relatives:			
RT	evidence from the globulin-1 gene.";			
RL	Genetics 0:0-0(1998).			
DR	EMBL; AF064220; AAC31463.1; -.			
DR	HSSP; P50477; 1CAU.			
DR	INTERPRO; IPR000901; -.			
DR	INTERPRO; IPR001113; -.			
DR	PRAM; PR00546; Seedstore_7s; 1			
DR	PROSITE; PS00867; CPASASE_2; UNKNOWN_1.			
FT	NON_TER	240	240	
EQ	SEQUENCE	240 AA;	27492 MW;	ECC26326633DFFB9 CRC64;

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Query Match      35.3%; Score 135; DB 10; Length 240;
Best Local Similarity 36.2%; Pred. No. 2, 1e-08;
Matches 25; Conservative 16; Mismatches 22; Indels 6; Gaps 3;

0Y 2 DDEDDRGAGHSLLDQCVQCRQERPRYSNARCVQDECRDQ---QDGNHDEEEOGGRG 57
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
26 DDNNNNNGGNGSGGVCVRR--EDRPNNQPRQLEQCEERERKQERQERSNENDDRRGKSS 84
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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OY 58 WHGGEREE 66  
 Db 85 -EDEREREQ 92

# RESULT 9

ID 081251 PRELIMINARY; PRT; 242 AA.

AC 081251; 01-NOV-1998 (TREMBlrel. 08, Created)

DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)

DE 01-OCT-2000 (TREMBlrel. 15, Last annotation update)

OS Zea mays subsp. mays (maize).

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.

OX NCBI\_TaxID=4578;

RN [1]

RT "Speciation and domestication in maize and its wild relatives;

RL Genetics 0:0-0(1998).

DR EMBL: AF064214; AAC31457.1; -

DR HSSP: P50477; ICAU.

DR MENDEL: 31893; Zeama:1188;31893.

DR INTERPRO: IPR000901; -

DR PRAM: PF00546; Seedstore\_7s; 1.

DR PROSITE: PS00867; CPSASE\_2; UNKNOWN\_1.

FT NON\_TER 242

SO SEQUENCE 242 AA; 27860 MW; 913912DE924B0ADB CRC64;

Query Match 35.3%; Score 135; DB 10; Length 242;

Best Local Similarity 38.2%; Pred. No. 2.1e-08; Matches 26; Conservative 13; Mismatches 21; Indels 8; Gaps 3;

OY 2 DDEDDRGGSHLQCVORCQERPRYSNARCVOECRPDO----OQGRNHQEEGCGRG 57

Db 26 DDNNHHNGHSGKSGRCVRC-EDRPWHQRPRLCQCREREKREKQERGRHETDSSGSG-- 82

OY 58 WHGGEREE 65

Db 83 -SSEDERE 89

# RESULT 10

ID 09SBE6 PRELIMINARY; PRT; 242 AA.

AC 09SBE6; 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DE 01-OCT-2000 (TREMBlrel. 15, Last annotation update)

OS Zea mays subsp. parviglumis.

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.

OX NCBI\_TaxID=76912;

RN [1]

RT "Speciation and domestication in maize and its wild relatives;

RL Genetics 0:0-0(1998).

DR EMBL: AF064225; AAC31468.1; -

DR HSSP: P50477; ICAU.

DR INTERPRO: IPR001113; -

DR PFAM: PF00546; Seedstore\_7s; 1.

FT NON\_TER 242

SO SEQUENCE 242 AA; 27856 MW; 8E6DB2C9E45C6BAD CRC64;

Query Match 35.3%; Score 135; DB 10; Length 242;

Best Local Similarity 38.2%; Pred. No. 2.1e-08; Matches 26; Conservative 13; Mismatches 21; Indels 8; Gaps 3;

OY 2 DDEDDRGGSHLQCVORCQERPRYSNARCVOECRPDO----OQGRNHQEEGCGRG 57

Db 26 DDNNHHNGHSGKSGRCVRC-EDRPWHQRPRLCQCREREKREKQERGRHETDSSGSG-- 82

OY 58 WHGGEREE 65

Db 83 -SSEDERE 89

# RESULT 11

ID 041750 PRELIMINARY; PRT; 407 AA.

AC 041750; 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

DE 01-MAY-2000 (TREMBlrel. 13, Last annotation update)

OS Zea mays (Maize).

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.

OX NCBI\_TaxID=4577;

RN [1]

RT "Speciation and domestication in maize and its wild relatives;

RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.

DR EMBL: U28017; AAB60295.1; -

DR MENDEL: 11236; Zeama:1188;11236.

DR INTERPRO: IPR000901; -

DR PRAM: PF00546; Seedstore\_7s; 1.

DR PROSITE: PS00867; CPSASE\_2; UNKNOWN\_1.

FT NON\_TER 407

SO SEQUENCE 407 AA; 46684 MW; 285E3ADE3C22969F CRC64;

Query Match 35.3%; Score 135; DB 10; Length 407;

Best Local Similarity 36.2%; Pred. No. 3.3e-08; Matches 25; Conservative 16; Mismatches 22; Indels 6; Gaps 3;

OY 2 DDEDDRGGSHLQCVORCQERPRYSNARCVOECRPDO----OQGRNHQEEGCGRG 57

Db 26 DDNNHHNGHSGKSGRCVRC-EDRPWHQRPRLCQCREREKREKQERGRHETDSSGSG-- 84

OY 58 WHGGEREE 66

Db 85 -EDEREREQ 92

# RESULT 12

ID 09SBE5 PRELIMINARY; PRT; 238 AA.

AC 09SBE5; 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DE 01-OCT-2000 (TREMBlrel. 15, Last annotation update)

OS Zea luxurians (Teosinte).

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.

OX NCBI\_TaxID=15945;

RN [1]

RT "Speciation and domestication in maize and its wild relatives;

RL Genetics 0:0-0(1998).

DR EMBL: AF064231; AAC31474.1; -

DR HSSP: P50477; ICAU.

DR INTERPRO: IPR001113; -

DR PFAM: PF00546; Seedstore\_7s; 1.

FT NON\_TER 242

SO SEQUENCE 242 AA; 27856 MW; 8E6DB2C9E45C6BAD CRC64;

DR HSSP: P50477; 1CAU.  
 DR INTERPRO: IPR000901; -.  
 DR INTERPRO: IPR001113; -.  
 DR PFAM: PF00546; Seedstore\_7s; 1.  
 DR PROSITE: PS00867; CPSASE\_2; UNKNOWN\_1.  
 FT NON\_TER 238  
 SO SEQUENCE 238 AA; 27254 MW; FFEA7BA7BA425D68 CRC64;

Query Match 35.1%; Score 134; DB 10; Length 238;  
 Best Local Similarity 36.2%; Pred. No. 2.7e-08;  
 Matches 25; Conservative 15; Mismatches 21; Indels 8; Gaps 3;

QY 2 DDEDDRGGHSLQOCVORCRQRPYSHARCVOECRDDQ---OQGRHDEEFGGRG 57  
 || ||| :||:| :|| : ||::||::| : ||| :| |  
 Db 26 DDNNHHGHHKSGRCVARRC-EDRPWHQRPCLQECREEREKROERSRHEDRSGSG-- 82

QY 58 WHGGEREE 66  
 |||||  
 Db 83 -SSDEREQ 90

RESULT 13

Q9S6Z6 PRELIMINARY; PRT; 238 AA.

AC Q9S6Z6; 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
 DE GLOBULIN-1 (FRAGMENT).  
 OS Zea luxurians (Teosinte).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.  
 OX NCBI\_TaxId=15945;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hilton H., Gaut B.S.;  
 RT "Speciation and domestication in maize and its wild relatives:  
 evidence from the globulin-1 gene.";  
 RL Genetics 0:0-0(1998).  
 DR EMBL: AF064232; AAC31475.1; -.  
 DR EMBL: AF064227; AAC31470.1; -.  
 DR EMBL: AF064230; AAC31473.1; -.  
 DR HSSP: P50477; 1CAU.  
 DR INTERPRO: IPR000901; -.  
 DR INTERPRO: IPR001113; -.  
 DR PRAM: PF00546; Seedstore\_7s; 1.  
 DR PROSITE: PS00867; CPSASE\_2; UNKNOWN\_1.  
 FT NON\_TER 238  
 SO SEQUENCE 238 AA; 27271 MW; FFE2169616319268 CRC64;

Query Match 35.1%; Score 134; DB 10; Length 238;  
 Best Local Similarity 36.2%; Pred. No. 2.7e-08;  
 Matches 25; Conservative 15; Mismatches 21; Indels 8; Gaps 3;

QY 2 DDEDDRGGHSLQOCVORCRQRPYSHARCVOECRDDQ---OQGRHDEEFGGRG 57  
 || ||| :||:| :|| : ||::||::| : ||| :| |  
 Db 26 DDNNHHGHHKSGRCVARRC-EDRPWHQRPCLQECREEREKROERSRHEDRSGSG-- 82

QY 58 WHGGEREE 66  
 |||||  
 Db 83 -SSDEREQ 90

RESULT 14

O81258 PRELIMINARY; PRT; 238 AA.

AC O81258; 01-NOV-1998 (TREMBlrel. 08, Created)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
 DE GLOBULIN-1 (FRAGMENT).

OS Zea luxurians (Teosinte).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.  
 OX NCBI\_TaxId=15945;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hilton H., Gaut B.S.;  
 RT "Speciation and domestication in maize and its wild relatives:  
 evidence from the globulin-1 gene.";  
 RL Genetics 0:0-0(1998).  
 DR EMBL: AF064229; AAC31472.1; -.  
 DR HSSP: P50477; 1CAU.  
 DR MENDEL: 31900; Zealu; 1188; 31900.  
 DR INTERPRO: IPR001113; -.  
 DR PFAM: PF00546; Seedstore\_7s; 1.  
 FT NON\_TER 238  
 SO SEQUENCE 238 AA; 27306 MW; BCA3CB36F28C6E2 CRC64;

Query Match 34.8%; Score 133; DB 10; Length 238;  
 Best Local Similarity 36.2%; Pred. No. 3.5e-08;  
 Matches 25; Conservative 15; Mismatches 21; Indels 8; Gaps 3;

QY 2 DDEDDRGGHSLQOCVORCRQRPYSHARCVOECRDDQ---OQGRHDEEFGGRG 57  
 || ||| :||:| :|| : ||::||::| : ||| :| |  
 Db 26 DDNNHHGHHKSGRCVARRC-EDRPWHQRPCLQECREEREKROERSRHEDRSGSG-- 82

QY 58 WHGGEREE 66  
 |||||  
 Db 83 -SSDEREQ 90

Query Match 34.8%; Score 133; DB 10; Length 238;  
 Best Local Similarity 36.2%; Pred. No. 3.5e-08;  
 Matches 25; Conservative 15; Mismatches 21; Indels 8; Gaps 3;

QY 2 DDEDDRGGHSLQOCVORCRQRPYSHARCVOECRDDQ---OQGRHDEEFGGRG 57  
 || ||| :||:| :|| : ||::||::| : ||| :| |  
 Db 26 DDNNHHGHHKSGRCVARRC-EDRPWHQRPCLQECREEREKROERSRHEDRSGSG-- 82

QY 58 WHGGEREE 66  
 |||||  
 Db 83 -SSDEREQ 90

RESULT 15

O81252 PRELIMINARY; PRT; 240 AA.

AC O81252; 01-NOV-1998 (TREMBlrel. 08, Created)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
 DE GLOBULIN-1 (FRAGMENT).  
 OS Zea mays subsp. mays (maize).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.  
 OX NCBI\_TaxId=4578;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hilton H., Gaut B.S.;  
 RT "Speciation and domestication in maize and its wild relatives:  
 evidence from the globulin-1 gene.";  
 RL Genetics 0:0-0(1998).  
 DR EMBL: AF064215; AAC31458.1; -.  
 DR HSSP: P50477; 1CAU.  
 DR MENDEL: 31894; Zeama; 1188; 31894.  
 DR INTERPRO: IPR000901; -.  
 DR INTERPRO: IPR001113; -.  
 DR PFAM: PF00546; Seedstore\_7s; 1.  
 DR PROSITE: PS00867; CPSASE\_2; UNKNOWN\_1.  
 FT NON\_TER 240  
 SO SEQUENCE 240 AA; 27560 MW; 5F54BC5CB06A983D CRC64;

Query Match 34.8%; Score 133; DB 10; Length 240;  
 Best Local Similarity 36.2%; Pred. No. 3.5e-08;  
 Matches 25; Conservative 15; Mismatches 23; Indels 6; Gaps 3;

QY 2 DDEDDRGGHSLQOCVORCRQRPYSHARCVOECRDDQ---OQGRHDEEFGGRG 57  
 || ||| :||:| :|| : ||::||::| : ||| :| |  
 Db 26 DDNNHHGHHKSGRCVARRC-EDRPWHQRPCLQECREEREKROERSRHEDRSGSGSS 84

QY 58 WHGGEREE 66  
 |||||  
 Db 85 -EDDEREQ 92

Search completed: March 1, 2001, 16:17:16  
job time: 454 sec

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